

09/508745

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- 31 -

SEQUENCE LISTING
SAC

(I) GENERAL INFORMATION:

(i) APPLICANT: (US ONLY): S. CORY, J.A. ADAMS, C. PRINT, L. GIBSON
(OTHER THAN US) THE WALTER AND ELIZA HALL INSTITUTE
OF MEDICAL RESEARCH

(ii) TITLE OF INVENTION: A METHOD OF TREATMENT AND AN ANIMAL
MODEL USEFUL FOR SAME

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DAVIES COLLISON CAVE
(B) STREET: 1 LITTLE COLLINS STREET
(C) CITY: MELBOURNE
(D) STATE: VICTORIA
(E) COUNTRY: AUSTRALIA
(F) ZIP: 3000

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT INTERNATIONAL
(B) FILING DATE: 16-SEP-1998

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PO9228
(B) FILING DATE: 16-SEP-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: HUGHES, DR E JOHN L
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(C) TELEX: AA 31787

WO 99/13710

- 32 -

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 582 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|---|-----|
| ATG GCG ACC CCA GCC TCG GCC CCA GAC ACA CGG GCT CTG GTG GCA GAC Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp 1 5 10 15 | 48 |
| TTT GTA GGT TAT AAG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GCC Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly 20 25 30 | 96 |
| CCC GGG GAG GGC CCA GCA GCT GAC CCG CTG CAC CAA GCC ATG CGG GCA Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala 35 40 45 | 144 |
| GCT GGA GAT GAG TTC GAG ACC CGC TTC CGG CGC ACC TTC TCT GAT CTG Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu 50 55 60 | 192 |
| CGC GCT CAG CTG CAT GTG ACC CCA GGC TCA GCC CAA CAA CGC TTC ACC Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr 65 70 75 80 | 240 |
| CAG GTC TCC GAT GAA CTT TTT CAA GGG GGC CCC AAC TGG GGC CGC CTT Gln Val Ser Asp Glu Leu Phe Gln Gly Pro Asn Trp Gly Arg Leu 85 90 95 | 288 |
| GTA GCC TTC TTT GTC TTT GGG GCT GCA CTG TGT GCT GAG AGT GTC AAC Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn 100 105 110 | 336 |
| AAG GAG ATG GAA CCA CTG GTG GGA CAA GTG CAG GAG TGG ATG GTG GCC Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala 115 120 125 | 384 |
| TAC CTG GAG ACG CGG CTG GCT GAC TGG ATC CAC AGC AGT GGG GGC TGG Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp 130 135 140 | 432 |
| CGG GAG TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GAG GCG CGG Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Ala Arg 145 150 155 160 | 480 |
| CGT CTG CGG GAG GGG AAC TGG GCA TCA GTG AGG ACA GTG CTG ACG GGG Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly 165 170 175 | 526 |
| GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser 180 185 190 | 576 |
| AAG TG Lys | 582 |

- 33 -

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp
1 5 10 15
Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
20 25 30
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
35 40 45
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
50 55 60
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
65 70 75 80
Gln Val Ser Asp Glu Leu Phe Gln Gly Pro Asn Trp Gly Arg Leu
85 90 95
Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
100 105 110
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
115 120 125
Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
130 135 140
Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Ala Arg
145 150 155 160
Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
165 170 175
Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
180 185 190
Lys

- 34 -

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 582 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | |
|---|-----|
| ATG GCG ACC CCA GCC TCA ACC CCA GAC ACA CGG GCT CTA GTG GCT GAC Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp 1 5 10 15 | 49 |
| TTT GTA GGC TAT AAG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GGC Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly 20 25 30 | 96 |
| CCT CGG GAA GGC CCA GCC GCC GAC CCG CTG CAC CAA GCC ATG CGG GCT Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala 35 40 45 | 144 |
| GCT GGA GAC GAG TTT GAG ACC CGT TTC CGC CGC ACC TTC TCT GAC CTG Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu 50 55 60 | 192 |
| GCC GCT CAG CTA CAC GTG ACC CCA CCC TCA GCC CAG CAA CGC TTC ACC Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr 65 70 75 80 | 240 |
| CAG GTT TCC GAC GAA CTT TTC CAA GGG GGC CCT AAC TGG CGG CGT CTT Gln Val Ser Asp Glu Leu Phe Gln Gly Pro Asn Trp Gly Arg Leu 85 90 95 | 288 |
| GTG GCA TTC TTT GTC TTT GGG GCT GCC CTG TGT GCT GAG AGT GTC AAC Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn 100 105 110 | 336 |
| AAA GAA ATG GAG CCT TTG GTG GGA CAA GTG CAG GAT TGG ATG GTG GCC Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Met Val Ala 115 120 125 | 384 |
| TAC CTG GAG ACA CGT CTG GCT GAC TGG ATC CAC AGC AGT GGG GGC TGG Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp 130 135 140 | 432 |
| GGC GAG TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GCA CGG Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Ala Arg 145 150 155 160 | 480 |
| CGT CTG CGG GAG GGG AAC TGG GCA TCA GTG AGG ACA GTG CTG ACG GGG Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly 165 170 175 | 528 |
| GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser 180 185 190 | 576 |
| AAG TG Lys | 562 |

- 35 -

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | |
|---|-----|
| Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp | 15 |
| 1 | 5 |
| Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly | 30 |
| 20 | 25 |
| Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala | 45 |
| 35 | 40 |
| Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu | 60 |
| 50 | 55 |
| Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr | 80 |
| 65 | 70 |
| Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu | 95 |
| 85 | 90 |
| Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn | 110 |
| 100 | 105 |
| Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Met Val Ala | 125 |
| 115 | 120 |
| Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp | 140 |
| 130 | 135 |
| Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg | 160 |
| 145 | 150 |
| Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly | 175 |
| 165 | 170 |
| Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser | 190 |
| 180 | 185 |
| Lys | |

- 36 -

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | |
|---|-----|
| ATG GCG ACC CCA GCC TCG CCC CCA GAC ACA CGG GCT CTG GTG GCA GAC Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp 1 5 10 15 | 48 |
| TTT GTA GGT TAT AAG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GGC Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly 20 25 30 | 96 |
| CCC GGG GAG GGC CCA GCA GCT GAC CCG CTG CAC CAA GCC ATG CGG GCA Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala 35 40 45 | 144 |
| GCT GGA GAT GAG TTC GAG ACC CGC TTC CGG CGC ACC TTC TCT GAT CTG Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu 50 55 60 | 192 |
| GCG GCT CAG CTG CAT GTG ACC CCA GGC TCA GCC CAG CAA CGC TTC ACC Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr 65 70 75 80 | 240 |
| CAG GTC TCC GAC GAA CTT TTT CAA GGG GGC CCC AAC TGG GGC CGC CTT Gln Val Ser Asp Glu Leu Phe Gln Gly Pro Asn Trp Gly Arg Leu 85 90 95 | 288 |
| GTA GCC TTC TCT TTT GGG GCT GCA CTG TGT GCT GAG AGT GTC AAC Val Ala Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn 100 105 110 | 336 |
| AAG GAG ATG GAA CCA CTG GTG GGA CAA GTG CAG GAG TGG ATG GTG GCC Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala 115 120 125 | 384 |
| TAC CTG GAG ACG CGG CTG GTC GAC TGG ATC CAC AGC AGT GGG GGC TGG Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp 130 135 140 | 432 |
| GCG GAG TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GAG GCG CGG Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Ala Arg 145 150 155 160 | 480 |
| CGT CTG CGG GAG GGG AAC TGG GCA TCA GTG AGG ACA GTG CTG ACG GGG Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly 165 170 175 | 528 |
| GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser 180 185 190 | 576 |
| AAG TGA A Lys * | 583 |

- 37 -

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 194 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp
1 5 10 15

Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
20 25 30

Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
35 40 45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
50 55 60

Ala Ala Gln Leu His val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
65 70 75 80

Gln Val Ser Asp Glu Leu Phe Gln Gly Pro Asn Trp Gly Arg Leu
85 90 95

Val Ala Phe Phe Leu Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
100 105 110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
115 120 125

Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp
130 135 140

Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
145 150 155 160

Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
165 170 175

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
180 185 190

Lys *

WO 99/13710

- 38 -

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 582 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | |
|---|---|
| ATG CCG ACC CCA GCC TCA ACC CCA GAC ACA CGC GCT CTA GTG GCT GAC | 48 |
| Met Pro Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp | |
| 1 5 | 10 15 |
| TTT GTA GGC TAT AGG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GGG | 96 |
| Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly | |
| 20 25 | 30 |
| CCT GGG GAA GGC CCA GCC GCC GAC CCG CTG CAC CAA GCC ATG CGG GCT | 144 |
| Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala | |
| 35 40 | 45 |
| GCT GGA GAC GAG TTT GAG ACC CGT TTC CGC CGC ACC TTC TCT GAC CTG | 192 |
| Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu | |
| 50 55 | 60 |
| GCC GCT CAG CTA CAC GTG ACC CCA GGC TCA GCC CAG CAA CGC TTC ACC | 240 |
| Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr | |
| 65 70 | 75 80 |
| CAG GTT TCC GAC GAA CTT TTC CAA GGG GCC CCT AAC TGG GGC CGT CTT | 288 |
| Gln Val Ser Asp Glu Leu Phe Gln Gly Pro Asn Trp Gly Arg Leu | |
| 85 90 | 95 |
| GTG GCA TTC TTT GTC TTT GGG GCT GCC CTG TGT GCT GAG AGT GTC AAC | 336 |
| Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn | |
| 100 105 | 110 |
| AAA GAA ATG GAG CCT TTG GTG GGA CAA GTC CAG GAT TGG ATC GTG GCC | 384 |
| Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala | |
| 115 120 | 125 |
| TAC CTG GAG ACA CGT CTG GCT GAC TGG ATC CAC AGC AGT GGC GGC TGG | 432 |
| Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp | |
| 130 135 | 140 |
| GCG GAC TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GAC GCA CGG | 480 |
| Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg | |
| 145 150 | 155 160 |
| CGT CTG CGG GAG GGC AAC TGG GCA TGA GTG AGC ACA GTG GTG ACG GGG | 528 |
| Arg Leu Arg Glu Gly Asn Trp Ala Val Ser Thr Val Val Thr Gly | |
| 165 170 | 175 |
| GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC | 576 |
| Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser | |
| 180 185 | 190 |
| AAG TG | 582 |
| Lys | |

- 39 -

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Thr | Pro | Ala | Ser | Thr | Pro | Asp | Thr | Arg | Ala | Leu | Val | Ala | Asp |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Phe | Val | Gly | Tyr | Arg | Leu | Arg | Gln | Lys | Gly | Tyr | Val | Cys | Gly | Ala | Gly |
| | | | | | | | | 25 | | | | | 30 | | |
| Pro | Gly | Glu | Gly | Pro | Ala | Ala | Asp | Pro | Leu | His | Gln | Ala | Met | Arg | Ala |
| | | | | | | | 40 | | | | | 45 | | | |
| Ala | Gly | Asp | Glu | Phe | Glu | Thr | Arg | Phe | Arg | Arg | Thr | Phe | Ser | Asp | Leu |
| | | | | | | 55 | | | | 60 | | | | | |
| Ala | Ala | Gln | Leu | His | Val | Thr | Pro | Gly | Ser | Ala | Gln | Gln | Arg | Phe | Thr |
| | | | | | 70 | | | | | 75 | | | 80 | | |
| Gln | Val | Ser | Asp | Glu | Leu | Phe | Gln | Gly | Gly | Pro | Asn | Trp | Gly | Arg | Leu |
| | | | | | | 85 | | 90 | | | | | 95 | | |
| Val | Ala | Phe | Phe | Val | Phe | Gly | Ala | Ala | Leu | Cys | Ala | Glu | Ser | Val | Asn |
| | | | | | | 100 | | | 105 | | | 110 | | | |
| Lys | Glu | Met | Glu | Pro | Leu | Val | Gly | Gln | Val | Gln | Asp | Trp | Ile | Val | Ala |
| | | | | | | 115 | | 120 | | | | 125 | | | |
| Tyr | Leu | Glu | Thr | Arg | Leu | Ala | Asp | Trp | Ile | His | Ser | Ser | Gly | Gly | Trp |
| | | | | | | 130 | | 135 | | | 140 | | | | |
| Ala | Asp | Phe | Thr | Ala | Leu | Tyr | Gly | Asp | Gly | Ala | Leu | Glu | Asp | Ala | Arg |
| | | | | | | 145 | | 150 | | | 155 | | 160 | | |
| Arg | Leu | Arg | Glu | Gly | Asn | Trp | Ala | * | Val | Ser | Thr | Val | Val | Thr | Gly |
| | | | | | | 165 | | | 170 | | | 175 | | | |
| Ala | Val | Ala | Leu | Gly | Ala | Leu | Val | Thr | Val | Gly | Ala | Phe | Phe | Ala | Ser |
| | | | | | | 180 | | | 185 | | | 190 | | | |
| Lys | | | | | | | | | | | | | | | |